

```

1 MPARRLLLLTLLPGLGIFGSTSTVTLPETLLFVSTLDGSLHAVSKRTG 50
  |||||
1 MPARRLLLLTLLPGLGIFGSTSTVTLPETLLFVSTLDGSLHAVSKRTG 50

51 SIKWTLKEDPVLQVPTHVEEPAFLDPDPNDGSLYTLGSKNNEGLTKLPFTI 100
  |||||
51 SIKWTLKEDPVLQVPTHVEEPAFLDPDPNDGSLYTLGSKNNEGLTKLPFTI 100

101 PELVQASPCRSSDGILYMGKKQDIWYVIDLLTGEKQQLSSAFADSLCPS 150
  |||||
101 PELVQASPCRSSDGILYMGKKQDIWYVIDLLTGEKQQLSSAFADSLCPS 150

151 TSLLYLGRTEYITIMYDTKTRELNRNATYFDYAASLPEDEGDYKMSHFVS 200
  |||||
151 TSLLYLGRTEYITIMYDTKTRELNRNATYFDYAASLPEDEGDYKMSHFVS 200

201 NGDGLVVTVDSESGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVETL 250
  |||||
201 NGDGLVVTVDSESGDVLWIQNYASPVVAFYVWQREGLRKVMHINVAVETL 250

```

THE

```

251 RYLTFMSGEVGRITKWKYFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300
|||||
251 RYLTFMSGEVGRITKWKYFPKETEAKSKLTPTLYVGKYSTSLYASPSMV 300

301 HEGVAVPRGSTPLLEGPQTDGVTIGDKGECVITPSTDVKFDPGLKSKN 350
|||||
301 HEGVAVPRGSTPLLEGPQTDGVTIGDKGECVITPSTDVKFDPGLKSKN 350

351 KNLNLRNYWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKS F 400
|||||
351 KNLNLRNYWLLIGHHETPLSASTKMLERFPNNLPKHRENVIPADSEKKS F 400

401 EE..TLLQMTS 409
|| :|::||
401 EEVINLVDQTS 411

```

FIG. 1 (CONT.)¹)

```

5  QLQSVSSAIHLCDKKMELSLNIPVNHGPQEESGSSQLHENSOSPETS  54
   :|||||
313 QLQSVSSAIHLCDKKMELSLNIPVNHGPQEESGSSQLHENSOSPETS  362
      .
55  SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSDSTISGSQRAAFCDHKTT  104
      |||||
363 SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSDSTISGSQRAAFCDHKTT  412
      .
105 PCSSAIINPLSTAGNSERLQPGIAQQWIIQSKREDIVNQMTACLNQSLDA  154
      |||||
413 PCSSAIINPLSTAGNSERLQPGIAQQWIIQSKREDIVNQMTACLNQSLDA  462
      .
155 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIQKLKDN  204
      |||||
463 LLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIQKLKDN  512
      .
      205 KQMGLOPYPEILVVSRSPSLNLLQNKSM  232
          |||||
      513 KQMGLOPYPEILVVSRSPSLNLLQNKSM  540

```

FIG. 2

```

1  MADLEAVLADVSYLMAMEKSKATPAARASKILLPEPSIRSVMQYLEDR 50
  |||||
1  MADLEAVLADVSYLMAMEKSKATPAARASKILLPEPSIRSVMQYLEDR 50
  |||||

51 GEVTFEKIFSQKLGYLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEE 100
  |||||
51 GEVTFEKIFSQKLGYLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEE 100
  |||||

101 RVARREIFDSYIMKELLACSHPFKSATEHVQGHGKQVPPDLFQPYI 150
  |||||
101 RVARREIFDSYIMKELLACSHPFKSATEHVQGHGKQVPPDLFQPYI 150
  |||||

151 EEICQNLRGDDVFQKFIE 167
  |||||
151 EEICQNLRGDDVFQKFIE 167
  |||||

```

FIG. 3


```

250 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRLSLPRLIDMSAQIAEGMAY 299
    |||||
301 AVVTKEPIYIVTEYMARGCLLDFLKTDEGSRLSLPRLIDMSAQIAEGMAY 350
    |||||

300 IERMNSIHRDLRAANILVSEALCCKIADFGGLARIIDSEYTAQEGAKFFPIK 349
    |||||
351 IERMNSIHRDLRAANILVSEALCCKIADFGGLARIIDSEYTAQEGAKFFPIK 400
    |||||

350 WTAPEAIHFGVFTIKADVWSFGVLLMEVVITYGRVPYPGMSNPEVIRNLER 399
    |||||
401 WTAPEAYHFGVFTIKADVWSFGVLLMEVVITYGRVPYPGMSNPEVIRNLER 450
    |||||

400 GYRMPRPDTCPPPELYRGVIAECWRSRPEERPTFFFLQSVLEDFYTATERQ 449
    |||||
451 GYRMPRPDTCPPPELYRGVIAECWRSRPEERPTFFFLQSVLEDFYTATERQ 500
    |||||

450 YELQP 454
    |||||
501 YELQP 505

```

FIG. 4 (CONT.)

[illegible]

FIG. 5

1 MTRDEALPDSHAQDFYENYEPKEILGRGVSSVRRRCIHKPTSQEYAVKV 50
 |||||
 1 MTRDEALPDSHAQDFYENYEPKEILGRGVSSVRRRCIHKPTSQEYAVKV 50
 51 IDVTGGGSFSPPEEVRRELREATLKEVDILRKVSGHPNISIQLKDTYETNTF 100
 |||||
 51 IDVTGGGSFSPPEEVRRELREATLKEVDILRKVSGHPNI.IQLKDTYETNTF 99
 101 FFLVFDLMKRGELED 115
 |||||
 100 FFLVFDLMKRGELED 114

FIG. 6

22 AVGCILAEALLAHRPLLPGTSEIHQIDLIVQLLGTSPSENIWPGFSKLPVLG 71
 |||||
 197 AVGCILAEALLAHRPLLPGTSEIHQIDLIVQLLGTSPSENIWPGFSKLPVLG 246
 72 QYSLRKQPYNNLKHKFPWLSEAGRLRLHFLFMYDPKKRATAGDCLESSYF 121
 |||||
 247 QYSLRKQPYNNLKHKFPWLSEAGRLRLHFLFMYDPKKRATAGDCLESSYF 296
 122 KEKPLRLPISGVCEGCREPG 141
 |||||
 297 KEKPLRLPISGVCEGCREPG 316

FIG. 8

1 MGEAEKFHYIYSCDLINVLKIGSLEGRKREQSKYKAVLEDPMLKFSGLY 50
 |||||
 1 MGEAEKFHYIYSCDLINVLKIGSLEGRKREQSKYKAVLEDPMLKFSGLY 50

51 QETCSDLYVTCQVFAEGKPLALPVRTSYKAFSTRWNWNEWLKLVPKYDDL 100
 |||||
 51 QETCSDLYVTCQVFAEGKPSALPVRTSYKAFSTRWNWNEWLKLVPKYDDL 100

101 PRNAQVALTIWDVYGPCKAVPVGGTTVSLFGKYGMFRQGMHDLKVWPVNE 150
 |||||
 101 PRNAQVALTIWDVYGPCKAVPVGGTTVSLFGKYGMSRQGMHDLKVWPVNE 150

151 ADGSEPTKTPGRTSSTLSEDQMSRLAKLTKAHRQGHMVVDWLDRLTFRE 200
 |||||
 151 ADGSEPTNTPGRTSSTLSEDQMSRLAKLTKAHRQGHMVVDWLDRLTFRE 200

201 IEMINESVKRSSNFMVLMGGFRCVKCDDKEYGIVVYEKDGDESSPILTSF 250
 |||||
 201 IEMINESVKRSSNFMVLMGGFRCVKCDDKEYGIVVYEKDGDESSPILTSF 250

251 ELVKVPDPQMSLENLVESKHHNLPRLSRGSPSDHDLKPYPSPRDQLKNIV 300
 |||||
 251 ELVKVPDPQMSLENLVESKHHNLPRLSRGSPSDHDLKPYPSPRDQLKNIV 300

FIG. 10

301 SYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIWDLPQEAQALA 350
 |||||
 301 SYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIWDLPQGAQALA 350

 351 LLGKWNPMDEVDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLLQLV 400
 |||||
 351 LLGKWNPMDEVDSLELISSHYTNPTVRRYAVARLRQADDEDLLMYLSQLV 400

 401 QALKYENFDDIKNGLEPTKKDSQSSVSENVSNGINSAEIDSSQIITSPL 450
 |||||
 401 QALKYENFDDIKNGLEPTKKDSQSSVSGNVSNNGINSAEIDSSQIITSPL 450

 451 PSVSSPPASKTKEVPDGENLEQDLCTFLISRACKNSTLANLYWYVIVE 500
 |||||
 451 PSVSSPPASKTKEVPDGENLEQDLCTFLISRASKNSTLANLYWYVIVE 500

 501 CEDQDTQQRDPKTHEMYLNVMRFRSQALLKGDKSVRMRSLLAAQQTFVD 550
 |||||
 501 CEDQDTQQRDPKTHEMYLNVMRFRSQALLKGDKSVRMRSLLAAQQTFVD 550

FIG. 10 (CONT.¹)

551	RLVHLMKAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK	600
551	RLVHLMKAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK	600
601	IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRRDQLILQI	650
601	IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRRDQLILQI	650
651	ISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSVPAEVLDTEGSI	700
651	ISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSVPAEVLDTEGSI	700
701	QNFFRKYAPSENGPNGISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLL	750
701	QNFFRKYAPSENGPNGISAEVMDTYVKSCAGYCVITYILGVGDRHLDNLLV	750
	751 LTKTG 755	
	751 LTKTG 755	

FIG. 10 (CONT.²)

```

1 MGEAEKFHYIYSCDLDINVLKIGSLEKREQKSYKAVLEDPMLKFSGLY 50
|||||
1 MGEAEKFHYIYSCDLDINVLKIGSLEKREQKSYNAVLEDPMLKFSGLY 50
|||||

51 QETCSDLYVTCQVFAEGKPLALPVRTSYKAFSTRWNNEWLKLVPKYDDL 100
|||||
51 QETCSDLYVTCQVFAEGKPSALPVRTSYKAFSTRWNNEWLKLVPKYDDL 100
|||||

101 PRNAQVALTIWDVYGP GKAVPGGTTVSLFGKYGMFRQGMHDLKVWPVNE 150
|||||
101 PRNAQVALTIWDVYGP GKAVPGGTTVSLFGKYGMSRQGMHDLKVWPVNE 150
|||||

151 ADGSEPTKTPGRTSSTLSEDDQMSRLAKLTKAHRQGMVKVDWLDRLTFRE 200
|||||:|||||
151 ADGSEPTNTPGRTSSTLSEDDQMSRLAKLTKAHRQGMVKVDWLDRLTFRE 200
|||||

201 IEMINESVKRSSNFMVYLMGGFRCVKCDDKEYGIVYYEKDGEDESSPILTSF 250
|||||
201 IEMINESVKRSSNFMVYLMGGFRCVKCDDKEYGIVYYEKDGEDESSPILTSF 250
|||||

251 ELVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDCLKPYSPRDQLKNIV 300
|||||
251 ELVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDCLKPYSPRDQLKNIV 300
|||||

```

FIG. 11


```

1  MGNAAAAGGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQFERIKTL 50
  |||||
1  MGNAAAAGGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDDQFERIKTL 50

51 GTGSFGRVMLVKHKETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVN 100
  |||||
51 GTGSFGRVMLVKHKETGNHYAMKILDQKVVKLKQIEHTLNEKRILQAVN 100

101 FPFLVKLEFSFKDNSNLYMVMEYVPGGEMFSLRRIGRF 139
  |||||
101 FPFLVKLEFSFKDNSNLYMVMEYVPGGEMFSLRRIGRF 139

```

FIG. 12

```

1  MVVFENGLLKICEAVSLKPTAWSLRHAVGPRPQTFLDPYIALNVDDSR 50
  |||||
1  MVVFENGLLKICEAVSLKPTAWSLRHAVGPRPQTFLDPYIALNVDDSR 50

. . .
51 IGQTATKQKTNPAWHDEFVTDVCNCRKIELAVFHDAPIGYDDFVANTCI 100
  |||||
51 IGQTATKQKTNPAWHDEFVTDVCNCRKIELAVFHDAPIGYDDFVANTCI 100

. . .
101 QFEELLQNGSRHFEDWIDLEPEGRVYVIIDLSSGSSGEVKIPNSAFCEER 150
  |||||
101 QFEELLQNGSRHFEDWIDLEPEGRVYVIIDLSSGSSGEAPKDNEERVFRER 150

151 VEMR 154
  :: |
151 MRPR 154

```

FIG. 13

1 MILIPRMLLVFLLLPILSSAKAQVNPAICRYPLGMSGGQIPDEDITASS 50
 |||||
 1 MILIPRMLLVFLLLPILSSAKAQVNPAICRYPLGMSGGQIPDEDITASS 50

 51 QWSESTAACYGRLDSEEGDGAWCPEIPVEPDDLKEFLQIDLHTLHFITLV 100
 |||||
 51 QWSESTAACYGRLDSEEGDGAWCPEIPVEPDDLKEFLQIDLHTLHFITLV 100

 101 GTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDI 150
 |||||
 101 GTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDI 150

 151 FLKDLPEPIVARFVRFIPVTDHSMNVCMRVELYGCVWLDGLVSNAPAGQ 200
 |||||
 151 FLKDLPEPIVARFVRFIPVTDHSMNVCMRVELYGCVWLDGLVSNAPAGQ 200

 201 QFVLPGGSIIYLNDVYDGAVGYSMTGLGQLTDGVSGLDDFTQTHEYHV 250
 |||||
 201 QFVLPGGSIIYLNDVYDGAVGYSMTGLGQLTDGVSGLDDFTQTHEYHV 250

 251 WPGYDYVGVWRNESATNGYIEIMFEEDRIRNFTTMKVHCNNMFAKGVKIFK 300
 |||||
 251 WPGYDYVGVWRNESATNGYIEIMFEEDRIRNFTTMKVHCNNMFAKGVKIFK 300

FIG. 14

301	EVQCYFRSEASEWEPNAISFPLVLDDVNPSAREFVTPLHHRMASAIKCQY	350
301	EVQCYFRSEASEWEPNAISFPLVLDDVNPSAREFVTPLHHRMASAIKCQY	350
351	HEADTWMFSEITFQSDAAMYNNSALPTSPMAPTTYDPMMLKVDDSNTRI	400
351	HEADTWMFSEITFQSDAAMYNNSALPTSPMAPTTYDPMMLKVDDSNTRI	400
401	LIGCLVAIIFILLAIIVILWRQWQKMLEKASRRMLDDEMTVSLSPSD	450
401	LIGCLVAIIFILLAIIVILWRQWQKMLEKASRRMLDDEMTVSLSPSD	450
451	SSMFNNRSPSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGEEE	500
451	SSMFNNRSPSPSEQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGEEE	500
501	SG.....EDDVVE.QGVKGETSASI	519
501	SGCSGVVKPVQPSGPEGVPHYAEADIVNLQGVTTGGNTYSV	540

FIG. 14 (CONT.¹)

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```

1 MANFQEHLSGSSPHLPFSESKTFNGLQDELTAMGNHSPKLEDQQKEG 50
|||||
1 MANFQEHLSGSSPHLPFSESKTFNGLQDELTAMGNHSPKLEDQQKEG 50

. . .
51 MVRTELIESVHSPVTTTTLTSVSEDSRDQFENSVLQRLREHDESETAVSQG 100
|||||
51 MVRTELIESVHSPVTTTTLTSVSEDSRDQFENSVLQRLREHDESETAVSQG 100

. . .
101 NSNTVDGESTGTEDIKIQFSRSGSGGFEGLFGCLRPVWNIIGKAYS 150
|||||
101 NSNTVDGESTGTEDIKIQFSRSGSGGFEGLFGCLRPVWNIIGKAYS 150

. . .
151 TDYKFMQQDTWEVPFEEISELQWLGSGAQGAVFLGKFRAEEVAIKKVREQ 200
|||:|||||
151 TDYKLQQQDTWEVPFEEISELQWLGSGAQGAVFLGKFRAEEVAIKKVREQ 200

. . .
201 NETDIKHLRKLKHPNIIAFKGVCTQAPCYCIIMEYCAHGQLYEVLGRK 250
|||||
201 NETDIKHLRKLKHPNIIAFKGVCTQAPCYCIIMEYCAHGQLYEVLGRK 250

. . .
251 ITPRLLVDWSTGIASGMNYLHLHKIIHRDLKSP 283
|||||
251 ITPRLLVDWSTGIASGMNYLHLHKIIHRDLKSP 283

```

FIG. 15

```

21 KSGNKS VH LRKASSPNLHRRQWEKNVPNTALTAENASILTSSLTAEDDR 70
   ::|||||
295 EKGNKS VH LRKASSPNLHRRQWEKNVPNTALTAENASILTSSLTAEDDR 344
   . . .
71 GGSVIKYSKN TTRKQWLKETPD TLLN ILKNADLSLAFQTYTYIRPGSEGF 120
   |||||||
345 GGSVIKYSKN TTRKQWLKETPD TLLN ILKNADLSLAFQTYTYIRPGSEGF 394
   . . .
121 LKGPLSEETEASD SV DGGHDSVILDPERLEPGLDEEDTD FEEEDDNP DWV 170
   |||||||
395 LKGPLSEETEASD SV DGGHDSVILDPERLEPGLDEEDTD FEEEDDNP DWV 444
   .
171 SELKKRAGWQGLCDR 185
   |||||||
445 SELKKRAGWQGLCDR 459

```

FIG. 16

```

1 MAPPEETPLIPQRSCSLLSTEAGALHVLLPARCGPPQRLSFG 46
  | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MAPPEETPLIPQRSCSLLSTEAGALHVLLPARCGPPQRLSFG 46

```

FIG. 17

```

1 MAESAGASSFFPLVLLLAGSGGSGPRGVQALLCACTSCLQANYTCETDG 50
  |||||
1 MAESAGASSFFPLVLLLAGSGGSGPRGVQALLCACTSCLQANYTCETDG 50

51 ACMVSI FNLDGMEHHVRTCIPKVELVPAGKPFYCLSSDLRNTHCCYTDY 100
  |||||
51 ACMVSI FNLDGMEHHVRTCIPKVELVPAGKPFYCLSSDLRNTHCCYTDY 100

101 CNRIDLRVPSGHLKEPEHPSMWGPVELVGIIAGPVFLLFLIIIVFLVIN 150
  |||||
101 CNRIDLRVPSGHLKEPEHPSMWGPVELVGIIAGPVFLLFLIIIVFLVIN 150

151 YHQRVYHNQRQLDMEDPSCMCLSKDKTQLQDLVYDLSTSGSGSGTKFF 198
  |||||
151 YHQRVYHNQRQLDMEDPSCMCLSKDKTQLQDLVYDLSTSGSGSGGLPLF 198

```

FIG. 18


```

1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50
  |||||
1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQSDVRIKFE 50

51 HNGERRIIAFSRPVKYEDVEHKVTTVFGQPLDLHYMNNELSILLKNQDDL 100
  |||||
51 HNGERRIIAFSRPVKYEDVEHKVTTVFGQPLDLHYMNNELSILLKNQDDL 100

101 DKAIDILDRSSMKSLRILLLSQDRNHNSSSPHSEVSRQVRIKASQASGD 150
  |||||
101 DKAIDILDRSSMKSLRILLLSQDRNHNSSSPHSEVSRQVRIKASQASGD 150

151 INTIYQPEPRSRHLSVSSQNPGRSSPPPGYVPERQQHIARQGSYTSINS 200
  |||||
151 INTIYQPEPRSRHLSVSSQNPGRSSPPPGYVPERQQHIARQGSYTSINS 200

201 EGEFIPETSEQCMLDPLSSAENSLSGSCQSLDRSADSPFVKSRMSRAQS 250
  |||||
201 EGEFIPETSEQCMLDPLSSAENSLSGSCQSLDRSADSPFVKSRMSRAQS 250

```

FIG. 19

```

251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRRTFFPRIR 300
|||||
251 FPDNRQEYSDRETQLYDKGVKGGTYPRRYHVSVHHKDYSDGRRTFFPRIR 300
|||||
301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRLSADSENALSVOERN 350
|||||
301 HQGNLFTLVPSSRSLSTNGENMGLAVQYLDPRGRLSADSENALSVOERN 350
|||||
351 VPTKCEELSLARRRLPRWSQTSYGGKQLG 379
|||| : ||
351 VPTKSPSAPINWRR.....GKLLG 369

```

FIG. 19 (CONT.¹)

```

1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQKKHNSSSS 50
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MDEQEALNSIMNDLVALQMNRRHRMPGYETMKNKDTGHSNRQ..... 42

51 ALLNSPTVTTSACAGASEKKKFLSDVRIKFEHNERRIIAFSRPVKYEDV 100
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
43 .....SDVRIKFEHNERRIIAFSRPVKYEDV 69

101 EHKVTVFGQPLDLHYMNNELSILLKNQDDLDKAIDILDRSSMKSLRIL 150
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
70 EHKVTVFGQPLDLHYMNNELSILLKNQDDLDKAIDILDRSSMKSLRIL 119

151 LLSQDRNHNSSPHSEVSQRVIKASQSAGDINTIYQPPEPRSRHLVSS 200
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
120 LLSQDRNHNSSPHSEVSQRVIKASQSAGDINTIYQPPEPRSRHLVSS 169

201 QNPGRSSPPGYVPERQQHIARQGSYTSINSEGEFIPETSEQCMLDPLSS 250
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
170 QNPGRSSPPGYVPERQQHIARQGSYTSINSEGEFIPETSEQCMLDPLSS 219

```

FIG. 20

```

251 AENSLGSCQSLDRSADSPFRKSRMSRAQFDPNQRQEYSDRETQLYDKG 300
    |||||
220 AENSLGSCQSLDRSADSPFRKSRMSRAQFDPNQRQEYSDRETQLYDKG 269
    .
301 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 350
    |||||
270 VKGGTYPRRYHVSVHHKDYSDGRRTFPRIRRHQGNLFTLVPSSRSLSTNG 319
    .
351 ENMGLAVQYLDPRGRLRSADSENALSVOERNVPTKCEELSLARRRLPRWS 400
    |||||
320 ENMGLAVQYLDPRGRLRSADSENALSVOERNVPTKSPSAPINWRR..... 364
    .
    401 QTSYGGKQLG 410
        || ||
    365 .....GKLLG 369

```

FIG. 20 (CONT.¹)

```

1 MAKQYDSVECPFCDEVSKYEKLAKIGQGTGFEVFKARHRKTGQKVALKKV 50
  |||||
1 MAKQYDSVECPFCDEVSKYEKLAKIGQGTGFEVFKARHRKTGQKVALKKV 50

. . .
51 LMENEKEGFPI TALREIKILQLLKHENVVNLI EICRTKASPNRCKGSIY 100
  |||||
51 LMENEKEGFPI TALREIKILQLLKHENVVNLI EICRTKASPNRCKGSIY 100

. . .
101 LVDFCEHDLAGLLSNVLVKFTLSEIKRVMQMLLNGLYY..... 139
  |||||
101 LVDFCEHDLAGLLSNVLVKFTLSEIKRVMQMLLNGLYYIHRNKILHRDM 150
. . .
139 ..... 139

151 KAA NVLITRDGVLKLADFG LARAFSLAKNSQPNRYTNRVVTLWYRPPPELL 200
. . .
139 ..... 139

201 LGERDYGPPI DLWGAGCIMAEMWTRSPIMQGNTEQHQLALISQLCGSITP 250
. . .

```

FIG. 21

```

139 ..... 139
251 EVWPNVDNYELYEKLVLKGGQKRKVKDRLKAYVRDPYALDLIDKLLVLDP 300
140 .....NHDFFWSDPMPSDLKGMLSTHLTSMFEYLAPPRKGSQIT 179
    |||||
301 AQRIDSDALNHDFFWSDPMPSDLKGMLSTHLTSMFEYLAPPRKGSQIT 350

    .
180 QQSTNQSRNPATTNQTEFERVF 201
    |||||
351 QQSTNQSRNPATTNQTEFERVF 372

```

FIG. 21 (CONT.¹)

FIG. 22

1 MATSRYPVAEIGVGAYGTVYKARDPHSGHFCALKSVRVP 40
| | | | | | | | | | | | | | | | | | | | | |
1 MATSRYPVAEIGVGAYGTVYKARDPHSGHFVALKSVRVP 40

FIG. 23

34 PLPLEPRAVYCKDVLIEQFSTVKGVNLDHTDDDFYSKFSTGVSIPWQN 83
|: :|||||||||||||||||||||||||||||||||||||
464 PFVPPRAVYCKDVLIEQFSTVKGVNLDHTDDDFYSKFSTGVSIPWQN 513
84 EMIETECFKELVFGPNGLPPDLNRNHPPEPPKGLLQRLFKRQHQNNS 133
|: :|||||||||||||||||||||||||||||||||||||
514 EMIETECFKELVFGPNGLPPDLNRNHPPEPPKGLLQRLFKRQHQNNS 563
134 KSSPSSKTSFNHHINSNHVSSNSTGSS 160
|: :|||||||||||||||||||||||||||||||||||||
564 KSSPSSKTSFNHHINSNHVSSNSTGSS 590

FIG. 24

```

28  LLSPSGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 77
   ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 LLDDYGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 367

78  YWGLGCLIIYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEEAK 127
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
368 YWGLGCLIIYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEEAK 417

128 SICKMLLTAKQRLGCGQEEGAAEVKRHPFFRNMFKRLEAGMLDPPFVP 177
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
418 SICKMLLTAKQRLGCGQEEGAAEVKRHPFFRNMFKRLEAGMLDPPFVP 467

178 DPRVYCKDVLIDIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPWQNEIE 227
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
468 DPRVYCKDVLIDIEQFSTVKGVNLDHTDDDFYSKFSTGSVIPWQNEIE 517

228 TECFKELNVFGPNGTLPDLNRNHPPEPPKGLLQRLFKRQHNNSSKSSP 277
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
518 TECFKELNVFGPNGTLPDLNRNHPPEPPKGLLQRLFKRQHNNSSKSSP 567

278 SSKTSFNHHHINSNHVSSNSTGSS 300
   ||||| ||||| ||||| ||||| |||||
568 SSKTSFNHHHINSNHVSSNSTGSS 590

```

FIG. 25

```

30 LLSPSGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 79
   ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 LLDDYGHIRISDLGLAVKIPEGDLIRGRVGTGYMAPEVLNNQRYGLSPD 367

   . . . . .
80 YWGLGCLYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEEA 129
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
368 YWGLGCLYEMIEGQSPFRGRKEKVKREEVDRRVLETEEVYSHKFSEEA 417

   . .
130 SICKMVSSWWPDATLKLVAPSLGLAPV 156
   ||||| : || :| :| :| :|
418 SICKMLLT..KDAKQRLGCQEEGAAEV 442

```

FIG. 26

```

1 MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50
  |||||
1 MAPFLRIAFNSYELGSLQAEDEANQPFCAVKMKEALSTERGKTLVQKKPT 50

51 MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPVSEVTGVSVLAERCKKNNG 100
  |||||
51 MYPEWKSTFDAHIYEGRVIQIVLMRAAEEPVSEVTGVSVLAERCKKNNG 100

101 KAEFWLDLQPQAKVLMVQYFLEDVDCKQSMRSEDEAKFPTMNRRAIAIKQ 150
  |||||
101 KAEFWLDLQPQAKVLMVQYFLEDVDCKQSMRSEDEAKFPTMNRRAIAIKQ 150

151 AKIHYIKNHEFIATFFGQPTFCSVCKDFVWGLNKQGYKCRQCNAAIHKKC 200
  |||||
151 AKIHYIKNHEFIATFFGQPTFCSVCKDFVWGLNKQGYKCRQCNAAIHKKC 200

201 IDKIIGRCTGTAANSRDTIFQKERFNIDMPHRFKVHNYSPTFCDHCGSL 250
  |||||
201 IDKIIGRCTGTAANSRDTIFQKERFNIDMPHRFKVHNYSPTFCDHCGSL 250

      .
251 LLPAPHDKHQW.....DCG 264
      |
251 L.....WGLVKQGLKCEDCG 265

```

FIG. 27

```

1 MDETHPGYGKEVDLEFLVSPSLPCLLSFAGSARHLVPPDSNLFSKLWACG 50
  |||||
203 MDETHPGYGKEVD.....LWACG 220

51 VILFTLLAGSPFWHRRQILMLRMIMEGYQFSSPEWDDRSSTVKDLISR 100
  |||||
221 VILFTLLAGSPFWHRRQILMLRMIMEGYQFSSPEWDDRSSTVKDLISR 270

101 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQRFRAVWTVLAAGR 150
  |||||
271 LLQVDPEARLTAEQALQHPFFERCEGSQPNLTPRQRFRAVWTVLAAGR 320

151 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWVKKEQQR 200
  |||||
321 VALSTHRVRPLTKNALLRDPYALRSVRHLIDNCAFRLYGHWVKKEQQR 370

201 AALFQHRPPGPPIMGPEEEGDSAAITDEAVLVLG 236
  |||||
371 AALFQHRPPGPPIMGPEEEGDSAAITDEAVLVLG 406

```

FIG. 28

```

1  MAFCAMRSSKKTEVNLEAPEPGVEVIFYLSDREPLRLGSGEYTAEELCI 50
  |||
1  MAFCAMRSSKKTEVNLEAPEPGVEVIFYLSDREPLRLGSGEYTAEELCI 50

51  RAAQACRISPLCHNLFALYDENTKLWYAPNRTITVDDKMSLRLHYRMRFY 100
  |||
51  RAAQACRISPLCHNLFALYDENTKLWYAPNRTITVDDKMSLRLHYRMRFY 100

101  FTNWHGTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG 150
  |||
101  FTNWHGTNDNEQSVWRHSPKKQKNGYEKKKIPDATPLLDASSLEYLFAQG 150

151  QYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMKKMQLPELP 200
  |||
151  QYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMKKMQLPELP 200

201  KDISYKRYIPETLNKSIRQRNLLTRMRINNVEKDFLKEFNNKTICDSSVS 250
  |||
201  KDISYKRYIPETLNKSIRQRNLLTRMRINNVEKDFLKEFNNKTICDSSVS 250

251  THDLKVKYLATLETLTCKHYGAEIFETSMLLISSENEMNWFHSNDGGNVLY 300
  |||
251  THDLKVKYLATLETLTCKHYGAEIFETSMLLISSENEMNWFHSNDGGNVLY 300

```

FIG. 29

[illegible]

FIG. 29 (CONT.)

1 MGCVQCKDEATKLTEERDGSLNQSSGARYGTDPQHYPSFGVTSIPNY 50
 |||||
 1 MGCVQCKDEATKLTEERDGSLNQSSGARYGTDPQHYPSFGVTSIPNY 50

 51 NNFHAAGGQGLTVFGGVNSSHTGTLRTRGGTGTFLFVALDYEARTEDD 100
 |||||
 51 NNFHAAGGQGLTVFGGVNSSHTGTLRTRGGTGTFLFVALDYEARTEDD 100

 101 LSFHKGEKFQILNSSEGDWWEARSLLTGETGYIPSNYVAPVDSIQAEWY 150
 |||||
 101 LSFHKGEKFQILNSSEGDWWEARSLLTGETGYIPSNYVAPVDSIQAEWY 150

 151 FGKLGKDAERQLLSFGNPRGTFLIRESSTTKGAYSLSIRDWDDMKGDHV 200
 |||||
 151 FGKLGKDAERQLLSFGNPRGTFLIRESSTTKGAYSLSIRDWDDMKGDHV 200

 201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250
 |||||
 201 KHYKIRKLDNGGYITTRAQFETLQQLVQHYSERAAAGLCCRLVVPCHKGM 250

 251 PRLLDLSVKTKDVWEIPRESLQLIKRLNGQGFGEVWMG 288
 |||||
 251 PRLLDLSVKTKDVWEIPRESLQLIKRLNGQGFGEVWMG 288

FIG. 30


```

1  MGCVQCKDEATKLT EERDGS LNQSSG RYGTDP TPQHYP SFVTSIPNY 50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MGCVQCKDEATKLT EERDGS LNQSSG RYGTDP TPQHYP SFVTSIPNY 50

51 NNFHAAGGQGLTV FGGVNSSS HTGTLR TRGGT VTLFVA LYDYEARTEDD 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 NNFHAAGGQGLTV FGGVNSSS HTGTLR TRGGT VTLFVA LYDYEARTEDD 100

101 LSFHKGEKFQIL NSSEG DWWEAR SLTTGE TGYIP SNYVAP VDSIQAE EWWY 150
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 LSFHKGEKFQIL NSSEG DWWEAR SLTTGE TGYIP SNYVAP VDSIQAE EWWY 150

151 FGKLGRKDAERQ LLSFGN PRGTFLI RESE TTKGAY SLSIR DWDDMK GDHV 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 FGKLGRKDAERQ LLSFGN PRGTFLI RESE TTKGAY SLSIR DWDDMK GDHV 200

201 KHYKIRKLDNGGY ITTRAQ FETLQQL VQHYSE RAAGLC CRLVVP CHKGM 250
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 KHYKIRKLDNGGY ITTRAQ FETLQQL VQHYSE RAAGLC CRLVVP CHKGM 250

```

FIG. 31

FIG. 31 (CONT.¹)

50 SLELHKRRKALTEPEARYYLRQIVLGCQYLHRNRVIHRDLKLGNLFLNE 99
 |||||
 137 SLELHKRRKALTEPEARYYLRQIVLGCQYLHRNRVIHRDLKLGNLFLNE 186
 . . .
 100 DLEVKIGDFGLATKVEYDGERKKTLCGTPNYIAPEVLSKKGHSEFVDVWS 149
 |||||
 187 DLEVKIGDFGLATKVEYDGERKKTLCGTPNYIAPEVLSKKGHSEFVDVWS 236
 . . .
 150 IGCIMYTLVVGKPPFETSCCLKETYLRIKKNEYSIPKHINPVAASLIQKML 199
 |||||
 237 IGCIMYTLVVGKPPFETSCCLKETYLRIKKNEYSIPKHINPVAASLIQKML 286
 . . .
 200 QTDPTARPTINELLNDEFFTSGYIPARLPITCLTIPPRFSIAPSSLDPSN 249
 |||||:|||||
 287 QTDPTARPTINELLGDEFFTSGYIPARLPITCLTIPPRFSIAPSSLDPSN 336
 . . .
 250 RKPLTVLNKGLENPLPERPREKEEPPVRETGEVVDCHLSDMLQQQLHSVNA 299
 |||||
 337 RKPLTVLNKGLENPLPERPREKEEPPVRETGEVVDCHLSDMLQQQLHSVNA 386
 . . .

FIG. 32

300 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSDKYGLGYQLCDNSVGVLF 349
 |||||
 387 SKPSERGLVRQEEAEDPACIPFWVSKWVDYSDKYGLGYQLCDNSVGVLF 436
 . . .
 350 NDSTRLLIYNDGDSLQYIERDGTESYLTVSSHPSNLSMKKITLLKYFRNYM 399
 |||||
 437 NDSTRLLIYNDGDSLQYIERDGTESYLTVSSHPSNLSMKKITLLKYFRNYM 486
 . . .
 400 SEHLLKAGANITPREGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 449
 |||||:|||||
 487 SEHLLKAGNITPRQGDELARLPYLRTWFRTRSAILHLNNGSVQINFFQ 536
 . . .
 450 DHTKLILCPLMAAVTYIDEKRDERTYRLSLEEYGCCKELASRLRYARTM 499
 |||||
 537 DHTKLILCPLMAAVTYIDEKRDERTYRLSLEEYGCCKELASRLRYARTM 586
 .
 500 VDKLLSSRSASNRLKAS 516
 |||||
 587 VDKLLSSRSASNRLKAS 603

FIG. 32 (CONT.¹)

FIG. 33

```

32 ERGLTVAFSILCNTLQPEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 81
   |: :: ::||: ||||| ||||| ||||| ||||| ||||| |||||
230 EKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 279
      .
      82 QGFSYDYVFDWNMLKFGASSQAQPRD 108
         ||||| ||||| ||||| : |:|
      280 QGFSYDYVFDWNMLKFGAARN...PED 303

```

FIG. 34

```

32 ERGLTVAFSILCNTLQPEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 81
   |: ::: :||: ||||| ||||| ||||| ||||| ||||| |||||
230 EKKMSTPIEVLCKGYPSEFSTYLNFCRSLRFDDKPDYSYLRQLFRNLFHR 279

   . . . . .
82 QGFSYDYVFDWNMLKFG.....GPL.SCQPPALP 109
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
280 QGFSYDYVFDWNMLKFGAARNPEDVDRERHEREERMQLRGSATRALP 329

   . . . . .
110 CGRPQDELGCSPESRGCGPGAAARTRTRGEDGAATGVDRDPSPAPWPTHGGH 159
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
330 PGPP.....TGATANRLRSAEPVASTPASRIQPA.....GN 361

   . . . . .
160 CQPAPQCRRGFHASLP.HPAGWQYFSQSDLAGR 193
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
362 TSPRAISRVDREKVMRLHRGAPANVSSSDLTGR 396

```

FIG. 35

167 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPPELPGGDDLKS 216
 |||
 1 MLPEDKEADSLRGNISVKAVKKEVEKKLRCLLADLPLPPELPGGDDLKS 50

217 PEEKKTATQLHSKRRPK 233
 |||
 51 PEEKKTTQLHSKRRPK 67

FIG. 36

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```

1 MSAKVRLKKLEQLLLDGPWRNESALS VETLLDVLVCLYTECSHSALRRDK 50
  |||||
1 MSAKVRLKKLEQLLLDGPWRNESALS VETLLDVLVCLYTECSHSALRRDK 50

51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIKVIGRGAFGEVAVVVKMKNTER 100
  |||||
51 YVAEFFLEWAKPFTQLVKEMQLHREDFEIIKVIGRGAFGEVAVVVKMKNTER 100

101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||||
101 IYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150

151 LVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAI DSIHQ LHYVHRD 200
  |||||
151 LVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAI DSIHQ LHYVHRD 200

201 IKPDNVLLDVNGHIRLADFGSCLKMND DGT VQSSVAVGTPDYISPEILQA 250
  |||||
201 IKPDNVLLDVNGHIRLADFGSCLKMND DGT VQSSVAVGTPDYISPEILQA 250

```

FIG. 37

```

251 MEDGMGKYGPEDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEERF 300
|||||
251 MEDGMGKYGPEDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEERF 300

301 QFPSHVTDVSEEAkdLIQRLSC 322
|||||
301 QFPSHVTDVSEEAkdLIQRLIC 322

```

FIG. 37 (CONT.¹)

```

1  MSAKVRLLKLEQLLLDGPWRNESALSVELLDVLVCLYTECSHSALRRDK 50
  |||||
1  MSAKVRLLKLEQLLLDGPWRNESALSVELLDVLVCLYTECSHSALRRDK 50

51 YVAEFLEWAKPFTQLVKEMQLHREDFEIIKVGAFGEVAVVKMKNTER 100
  |||||
51 YVAEFLEWAKPFTQLVKEMQLHREDFEIIKVGAFGEVAVVKMKNTER 100

101 IYAMKIILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150
  |||||
101 IYAMKIILNKWEMLKRAETACFREERDVLVNGDCQWITALHYAFQDENHLY 150

151 LVMDYYVVGDDLTLLSKFEDKLPEDMARFYIGEMVLAIIDSIHQHLYVHRD 200
  |||||
151 LVMDYYVVGDDLTLLSKFEDKLPEDMARFYIGEMVLAIIDSIHQHLYVHRD 200

201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231
  |||||
201 IKPDNVLLDVNGHIRLADFGSCLKMNDGTV 231

```

FIG. 38

1 MELRVGNRYRLGRKIGSGSGFDIYL..... 25
 |||||
 1 MELRVGNRYRLGRKIGSGSGFDIYLGTDIAAGEEVAIKLECVKTKHPQLH 50

 26VGIP TIRWCGAEGDYNVMVMELLGPSLEDLNFCSRKF 63
 |||||
 51 IESKIYKMMQGGVGIPTIRWCGAEGDYNVMVMELLGPSLEDLNFCSRKF 100

 64 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDF 113
 |||||
 101 SLKTVLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDF 150

 114 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLES LG 163
 |||||
 151 GLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRDDLES LG 200

 164 YVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 213
 |||||
 201 YVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFAT 250

FIG. 39

FIG. 39 (CONT.¹)

FIG. 40

264	RSRSGKFRLVTKFKKEKNKNKNEAHSSLGAPVHLWGTEEVAAWLEHLSLC	313
1066	RSRSGKFRLVTKFKKEKNKNKNEAHSSLGAPVHLWGTEEVAAWLEHLSLC	1115
314	EYKDIFTRHDIRGSELLHLERRDLKDLGVTKVGHMKRILCGIKELSRSA	363
1116	EYKDIFTRHDIRGSELLHLERRDLKDLGVTKVGHMKRILCGIKELSRSA	1165
	364 AVEA	367
	1166 AVEA	1169

FIG. 40 (CONT.¹)

```

1 MSDVAIVKEGWLHKGGEYIKTWRPRYFLKNDGTFIGYKERPQVDQREA 50
  |||||
1 MSDVAIVKEGWLHKGGEYIKTWRPRYFLKNDGTFIGYKERPQVDQREA 50
  . . .
51 PLNFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVETPEEREWT 100
  |||||
51 PLNFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVETPEEREWT 100
  . . .
101 TAIQTVADGLKKQEEEEEMDFRSGSPSDNSGAEEEMVSLAKPKHRVAL 147
  |||||
101 TAIQTVADGLKKQEEEEEMDFRSGSPSDNSGAEEEMVSLAKPKHRVTM 147

```

FIG. 41

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```

1 MIVHDDVESEPA MTPSKEGTLIVRQTQSASSTLQKHKSSSFTPFIDPRL 50
  |||
751 MIVHDDVESEPA MTPSKEGTLIVRQTQSASSTLQKHKSSSFTPFIDPRL 800

51 LQISPSSGTTVTSVVGFC DGM RPEAIRQDPTRKGSVVNVNPTNTRPQSD 100
  |||
801 LQISPSSGTTVTSVVGFC DGM RPEAIRQDPTRKGSVVNVNPTNTRPQSD 850

101 TPEIRKYKKRFNSEILCAALGWVNLLVGTESGLMLLDRSGQGVYPLINR 150
  |||
851 TPEIRKYKKRFNSEILCAALGWVNLLVGTESGLMLLDRSGQGVYPLINR 900

151 RRFQQMDVLEGLNVLVLTISGKKDKLRVYVYLSWLRNKILHNDPEVEKKQGW 200
  |||
901 RRFQQMDVLEGLNVLVLTISGKKDKLRVYVYLSWLRNKILHNDPEVEKKQGW 950

201 TTVGDLEGCVHYKVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSF 250
  |||
951 TTVGDLEGCVHYKVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSF 1000

```

FIG. 42

```

251  GELVHKPLLVDLTVEEGQRLKVIYGSCAGFHAVDVDSGSVDIYLPTHIQ 300
    |||||
1001 GELVHKPLLVDLTVEEGQRLKVIYGSCAGFHAVDVDSGSVDIYLPTHIQ 1050
    |||||

301  CSIKPHAIILPNTDGMELLVCYEDEGVYVNTYGRITKDVVLQWGENPTS 350
    |||||
1051 CSIKPHAIILPNTDGMELLVCYEDEGVYVNTYGRITKDVVLQWGENPTS 1100
    |||||

351  VAYIRSNQTMGWGEKAIEIRSVETGHLDDGVFMHKRAQRLKFLCERNDKVF 400
    |||||
1101 VAYIRSNQTMGWGEKAIEIRSVETGHLDDGVFMHKRAQRLKFLCERNDKVF 1150
    |||||

    401  FASVRSGGSSQVYFMTLGRTSLLSW 425
    |||||
    1151 FASVRSGGSSQVYFMTLGRTSLLSW 1175

```

FIG. 42 (CONT.¹)

14	GEVDLTALAKELRAVEDVRPPHKVTDYSSSEESGTTDEEDDDVEQEGAD	63
674	GEVDLTALAKELRAVEDVRPPHKVTDYSSSEESGTTDEEDDDVEQEGAD	723
64	ESTSGPEDTRAASSLNSNGETESVKTMI VHDDVESE PAMTPSKEGTLIV	113
724	ESTSGPEDTRAASSLNSNGETESVKTMI VHDDVESE PAMTPSKEGTLIV	773
114	RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR	163
774	RQTQSASSTLQKHKSSSFTPFIDPRLLQISPSSGTTVTSVVGFS CDGMR	823
164	PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV	213
824	PEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGV	873
214	NLLVGTESGLMLDRSGQGKVYPLINRRRFQQMDVLEGLNVLTISGKKD	263
874	NLLVGTESGLMLDRSGQGKVYPLINRRRFQQMDVLEGLNVLTISGKKD	923
264	KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERIKFL	313
924	KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGCVHYKVVKYERIKFL	973

FIG. 43

314 VIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLVDLTVEEGQRLKVI 363
 974 VIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLVDLTVEEGQRLKVI 1023
 364 YGSCAGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCY 413
 1024 YGSCAGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCY 1073
 414 EDEGVYVNTYGRITKDVVLQWGEPTSVAYIRSNQTMGWGEKAIEIRSVE 463
 1074 EDEGVYVNTYGRITKDVVLQWGEPTSVAYIRSNQTMGWGEKAIEIRSVE 1123
 464 TGHLDGVFMHKRAQRLKFLCERNQDKVFFASVRSGSSQVYFMTLGRTSLL 513
 1124 TGHLDGVFMHKRAQRLKFLCERNQDKVFFASVRSGSSQVYFMTLGRTSLL 1173

514 SW 515
 1174 SW 1175

FIG. 43 (CONT.¹)

```

64 LTANETQSASSTLQKHKSSSFTFIDPRLLQISPSSGTTVTSVVGFS CD 113
| ::::::::::::::::::::::::::::::::::::::::::::::::::::
771 LIVRQTQSASSTLQKHKSSSFTFIDPRLLQISPSSGTTVTSVVGFS CD 820

114 GMRPEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAAL 163
| ::::::::::::::::::::::::::::::::::::::::::::::::::::::
821 GMRPEAIRQDPTRKGSVVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAAL 870

164 WGVNLLVGTESGLMLLDRSGQGVYPLINRRRFQQMDVLEGLNVLVTISG 213
| ::::::::::::::::::::::::::::::::::::::::::::::::::::::
871 WGVNLLVGTESGLMLLDRSGQGVYPLINRRRFQQMDVLEGLNVLVTISG 920

214 KKD KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGECVHYKVVKYERI 263
| ::::::::::::::::::::::::::::::::::::::::::::::::::::::
921 KKD KLRVYYLSWLRNKILHNDPEVEKKQGWTTVGDLGECVHYKVVKYERI 970

264 KFLVIALKSSVEVYAWAPKPYHKFMFKSFGELVHKPLLVDLTVEEGQRL 313
| ::::::::::::::::::::::::::::::::::::::::::::::::::::::
971 KFLVIALKSSVEVYAWAPKPYHKFMFKSFGELVHKPLLVDLTVEEGQRL 1020

```

FIG. 44

FIG. 44 (CONT.¹)


```

251 LVPIGKSCNAGYEERGMQACRPGFYKALDGNMCKCAKCPHSSTQEDG 300
|||||
251 LVPIGKSCNAGYEERGMQACRPGFYKALDGNMCKCAKCPHSSTQEDG 300
|||||
301 SMNCRCENNYFRADKDPSPMACTRPSPSPRNVISNINETSVILDWSWPLD 350
|||||
301 SMNCRCENNYFRADKDPSPMACTRPSPSPRNVISNINETSVILDWSWPLD 350
|||||
351 TGGRKDVTFNII CKKCGWNIKQCEPCSPNVRF LPRQFGLTNTT VTVTDLL 400
|||||
351 TGGRKDVTFNII CKKCGWNIKQCEPCSPNVRF LPRQFGLTNTT VTVTDLL 400
|||||
401 AHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPVLT IKKDRTSR 450
|||||
401 AHTNYTFEIDAVNGVSELSSPPRQFAAVSITTNQAAPSPVLT IKKDRTSR 450
|||||
451 NSISLSWQEPHPNGIILDYEVKYYEKQEQETS YTILRARGTNVTISSLK 500
|||||
451 NSISLSWQEPHPNGIILDYEVKYYEKQEQETS YTILRARGTNVTISSLK 500
|||||

```

FIG. 45 (CONT.)¹⁾


```

501 PDIIYVFQIRARTAGYGTNSRKFEFETSPDSFSISGESSQVVMIAISAA 550
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501 PDIIYVFQIRARTAGYGTNSRKFEFETSPDSFSISGESSQVVMIAISAA 550

551 VAIILLTVVIYVLI GRFCGYKSKHGADEKRLHFGNGHLKLPGLRTYVDPH 600
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
551 VAIILLTVVIYVLI GRFCGYKSKHGADEKRLHFGNGHLKLPGLRTYVDPH 600

    601 TYEDPTQAVHEFAKELDATNISIDKVVGA 629
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    601 TYEDPTQAVHEFAKELDATNISIDKVVGA 629

```

FIG. 45 (CONT.²)

```

6   WGWVAVVKLNADKVFAMKIILNKWEMLKRAETACFREEERDVLVNGDNKWI  55
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
88  FGEVAVVKLNADKVFAMKIILNKWEMLKRAETACFREEERDVLVNGDNKWI  137

56  TTLHYAFQDDNNLYLVMDYVVGDDLTLLSKFEDRLPEDMARFYLAEMVI  105
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
138 TTLHYAFQDDNNLYLVMDYVVGDDLTLLSKFEDRLPEDMARFYLAEMVI  187

106 AIDSVHQHLHVHRDIKPDNIIILMDMNGHIRLADFGSCLKLMEDGTVQSSVA  155
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
188 AIDSVHQHLHVHRDIKPDNIIILMDMNGHIRLADFGSCLKLMEDGTVQSSVA  237

156 VGTPDYISPEILQAMEDKGGRYGPECDWWSLGVCMEMLYGETPFYAESL  205
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
238 VGTPDYISPEILQAMEDKGGRYGPECDWWSLGVCMEMLYGETPFYAESL  287

206 VETYCKIMNHKERFQFPAQVTDVSENAKDIIIRLLICSRHRLQGONGIEDF  255
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
288 VETYCKIMNHKERFQFPAQVTDVSENAKDIIIRLLICSRHRLQGONGIEDF  337

```

FIG. 46

256 KKHFFSGIDWNIRNCEAPYIPEVSSPTDTSNFDVDDDDCLKNSETMPPP 305
 |||||
 338 KKHFFSGIDWNIRNCEAPYIPEVSSPTDTSNFDVDDDDCLKNSETMPPP 387
 |||||
 306 THTAFSGHHLPFVGFTYTSSCVLSRCLRVTAGPTSLDLDVNVQRTLDN 355
 |||||
 388 THTAFSGHHLPFVGFTYTSSCVLSRCLRVTAGPTSLDLDVNVQRTLDN 437
 |||||
 356 NLATEAYERRIKRLEQEKLELSRKLQESTQTVQALQYSTVDGPLTASKDL 405
 |||||
 438 NLATEAYERRIKRLEQEKLELSRKLQESTQTVQALQYSTVDGPLTASKDL 487
 |||||
 406 EIKNLKEEI 414
 |||||
 488 EIKNLKEEI 496

FIG. 46 (CONT.¹)

```

1 MEVDPQQLGMFTGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLGKYL 50
  |||||
1 MEVDPQQLGMFTGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLGKYL 50
  .
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  |||||
51 MGDLLGEGSYGKVKEVLDSETLCRRRAVKILKKKKLRRIPNGEANVKKEIQ 100
  .
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPV 150
  |||||
101 LLRRLRHKNVIQLVDVLYNEEKQKMYMVMEYCVCGMQEMLDSVPEKRFPV 150
  .
151 CQAHG 155
  ||||
151 CQAHG 155

```

FIG. 47

FIG. 48

```

27 VKDFLSQLRSSNRFSIPESGQGGTEMDGFRRTIENQHRSRNDVMVSEWLN 76
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 VKDFLSQLKSSNRFSIPESGQGGTEMDGFRRTIENQHRSRNDVMVSEWLN 350
   . . . . .
77 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPE 126
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 KLNLEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPE 400
   . . . . .
127 TSTFRNQMPSTSTGTSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 176
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
401 TSTFRNQMPSTSTGTSPGPRGNQGAERQGMNWSCRTPEPNPVTGRPLV 450
   . . . . .
177 NIYNCSGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQHPPVGSQEGP 226
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
451 NIYNCSGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQHPPVGSQEGP 500
   .
      227 KDPEAWSRPQGWYNHSGK 244
         |||||:|||||:|||||:|||||:|||||:|||||:|||||
      501 KDPEAWSRPQGWYNHSGK 518

```

FIG. 49.

30 EEQARELYRRLREKPRDQTEGDSQEMVRLLLQAIQSFEEKVRVIYTQLS 79
 |||||
 564 EEQARELYRRLREKPRDQTEGDSQEMVRLLLQAIQSFEEKVRVIYTQLS 613
 . . .
 80 KTVVCKQKALELLPKVVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACS 129
 |||||
 614 KTVVCKQKALELLPKVVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACS 663
 . . .
 130 KVRGPVSGSPDSMNASRLSQPGQMSQPSTASNSLPEPAKSEELVAEAEH 179
 |||||
 664 KVRGPVSGSPDSMNASRLSQPGQMSQPSTASNSLPEPAKSEELVAEAEH 713
 . . .
 180 NLCTLLENAIQDTVREQDQSF TALDWSWLQTEEEHSCLEQAS 222
 |||||
 714 NLCTLLENAIQDTVREQDQSF TALDWSWLQTEEEHSCLEQAS 756

FIG. 50

```

1  MRLTLLCCTWREERMGEESLPCVASCGRQRIYDGQYLQALNADWHADCF 50
   |||||
1  MRLTLLCCTWREERMGEESLPCVASCGRQRIYDGQYLQALNADWHADCF 50

51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
   |||||
51 RCCDCSASLSHQYYEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

101 ELKYHPECFICLTGTFIGDGTYYLVEHSKLYCGHCYYQTVVTPVIEQI 150
   |||||
101 ELKYHPECFICLTGTFIGDGTYYLVEHSKLYCGHCYYQTVVTPVIEQI 150

151 LPDSPGSHLPHTVTLVSI PASSHGKRGSLVSIDPPHGPFGCGTEHSHTVR 200
   |||||
151 LPDSPGSHLPHTVTLVSI PASSHGKRGSLVSIDPPHGPFGCGTEHSHTVR 200

201 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250
   |||||
201 VQGVDPGCMSPDVKNLSIHVGDRILEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 51

251 QLTLEHDPHDTLGHGLPETSPSSPAYTPSGEAGSSARQKPVLRSCSID 300
 |||||
 251 QLTLEHDPHDTLGHGLPETSPSSPAYTPSGEAGSSARQKPVLRSCSID 300
 301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGCF 350
 |||||
 301 RSPGAGSLGSPASQQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLKGCF 350

351 GQAIKV 356

|||||

351 GQAIKV 356

FIG. 51 (CONT.¹)

```

1   MRLTLCCCTWREERMGEESLPCVASCGRIDYDGYLQALNADWHADCF  50
    |||||
1   MRLTLCCCTWREERMGEESLPCVASCGRIDYDGYLQALNADWHADCF  50

51  RCCDCSASLSHQYYEKDGQLFCKKDYWAYRGESCHGCSEQITKGLVMVAG  100
    |||||
51  RCCDCSASLSHQYYEKDGQLFCKKDYWAYRGESCHGCSEQITKGLVMVAG  100

101 ELKYHPECFICLTGTFIGDGDYTLVEHSKLYCGHCYYQTVVTPVIEQI  150
    |||||
101 ELKYHPECFICLTGTFIGDGDYTLVEHSKLYCGHCYYQTVVTPVIEQI  150

151 LPDSPGSHLPHTVTLVSIPASSHGKRGLSVSIDPPHPGCCGTEHSHTVR  200
    |||||
151 LPDSPGSHLPHTVTLVSIPASSHGKRGLSVSIDPPHPGCCGTEHSHTVR  200

201 VQGVDPGCMSPDVKNСИHVGDRILEINGTPIRNVPPLDEIDLIIQETSRL  250
    |||||
201 VQGVDPGCMSPDVKNСИHVGDRILEINGTPIRNVPPLDEIDLIIQETSRL  250

```

FIG. 51

```

. . .
251 QLTLEHDPHDTLGHGLGPETSPSSPAYTPSGEAGSSARQKPVLRSCSID 300
|||||
251 QLTLEHDPHDTLGHGLGPETSPSSPAYTPSGEAGSSARQKPVLRSCSID 300

. . .
301 RSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLGKGC 350
|||||
301 RSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLIHGEVLGKGC 350

351 GQAIKV 356
|||||
351 GQAIKV 356

```

FIG. 51 (CONT.¹)

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```

1 1 MRLTLLCCTWREERMGEESLPCVASCGRITYDGQYLQALNADWHADCF 50
  |||||
1 1 MRLTLLCCTWREERMGEESLPCVASCGRITYDGQYLQALNADWHADCF 50

51 1 RCCDCSASLSHQYEEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100
  |||||
51 1 RCCDCSASLSHQYEEKDGQLFCKKDYWARYGESCHGCSEQITKGLVMVAG 100

101 1 ELKYHPECFICLTGCTFIGDGDYTLVEHSKLYCGHCYQTVVTPVIEQI 150
  |||||
101 1 ELKYHPECFICLTGCTFIGDGDYTLVEHSKLYCGHCYQTVVTPVIEQI 150

151 1 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCGTEHSHTVR 200
  |||||
151 1 LPDSPGSHLPHTVTLVSI PASSHGKRGLSVSI DPHGPPGCGTEHSHTVR 200

201 1 VQGVDPGCMSPDVKN SIHVGDRI LEINGTPIRNVPLDEIDLLIQETSRL 250
  |||||
201 1 VQGVDPGCMSPDVKN SIHVGDRI LEINGTPIRNVPLDEIDLLIQETSRL 250

```

FIG. 52

301 LPSA 305

301 RSPGA 305

FIG. 52 (CONT.¹)

```

1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50
  |||||
1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50

51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100
  |||||
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100

101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150
  |||||
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150

151 TYSNGSTKDRKLLLTAAQQLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200
  |||||
151 TYSNGSTKDRKLLLTAAQQLQDSKTKIDIIRMQLRRALQAGQLENQAAPD 200

201 DTQGSPDLGAVELRIEELRRHHFRVEHAEGAKNVLLSAAKAPDRKAV 250
  |||||
201 DTQGSPDLGAVELRIEELRRHHFRVEHAEGAKNVLLSAAKAPDRKAV 250

```

FIG. 53

251 SEAQKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300
 |||||
 251 SEAQKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300
 . . .
 301 STRLAGFPFATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350
 |||||
 301 STRLAGFPFATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350
 . . .
 351 PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEENTSEVSTVLKLDNT 400
 |||||
 351 PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEENTSEVSTVLKLDNT 400
 . . .
 401 VVGQTSWKPCGPNAWDQSFTLELERARELELAVFWRDQRGLCALKFLKLE 450
 |||||
 401 VVGQTSWKPCGPNAWDQSFTLELERARELELAVFWRDQRGLCALKFLKLE 450
 . . .
 451 DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQGK 500
 |||||
 451 DFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQKKIFSKQQGK 500

FIG. 53 (CONT.¹)

[illegible]

FIG. 53 (CONT. 2)


```

723 ..... 723
751 EGYVKIADFGLCKEGMGYGDRSTFCGTPEFLAPEVLTDTSYTRAVDWWG 800
723 ..... 723
801 LGVLLYMLVGESPFPGDDEEEVFDSIVNDEVRYPRFLSAEAGIMRRLL 850
724 .....RLPPPFVPTLSGRD 738
      |||||
851 RRNPERRLGSSERDAEDVKKQPFRTLGWEALLARRLPPFPVPTLSGRD 900
      .
739 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDFDEVAGGC 780
      |||||
901 VSNFDEEFTGEAPTLSPPRDARPLTAAEQAAFLDFDEVAGGC 942

```

FIG. 53 (CONT.³)

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```

1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50
  |||||
1 MASDAVQSEPRWSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKEL 50

. . .
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100
  |||||
51 KLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLLDHLHQQLQELHAHVVL 100

. . .
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150
  |||||
101 PDPAATHDGPQSPGAGGPTCSATNLSRVAGLEKQLAIELKVKQGAENMIQ 150

. . .
151 TYSNGSTKDRKLLLTAAQQLQDSKTKIDIIRMQLRRALQADQLENQAAPD 200
  |||||
151 TYSNGSTKDRKLLLTAAQQLQDSKTKIDIIRMQLRRALQAGQLENQAAPD 200

. . .
201 DTQGSPDLGAVELRIEELRHHFRVEHVAEAGAKNVLLSAAKAPDRKAV 250
  |||||
201 DTQGSPDLGAVELRIEELRHHFRVEHVAEAGAKNVLLSAAKAPDRKAV 250

```

FIG. 54

```

251  SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300
|||||
251  SEAQEKLTESNQKLGLLREALERRLGELPADHPKGRLLREELAAASSAAF 300

301  STRLAGFPFATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350
|||||
301  STRLAGFPFATHYSTLCKPAPLTGTLEVRVVGCRDLPETIPWNPTPSMGG 350

351  PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEENTSEVSTVLKLDNT 400
|||||
351  PGTPDSRPPFLSRPARGLYSRGSLGRSSLKAEAEENTSEVSTVLKLDNT 400

```

FIG. 54 (CONT.¹)

FIG. 55

90 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELA~~KDFIR~~LLVKDP 139
 |||||
 211 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELA~~KDFIR~~LLVKDP 260
 |||||
 140 KRRMTIAQSL~~EH~~SWIKAIRRRNV~~RG~~EDSGRKPER~~RR~~LKTT~~RL~~KEYTIKSH 189
 |||||
 261 KRRMTIAQSL~~EH~~SWIKAIRRRNV~~RG~~EDSGRKPER~~RR~~LKTT~~RL~~KEYTIKSH 310
 |||||
 190 SSLPPNNSYADFERFSKVL~~EE~~AAAAEEGLRELQ~~RS~~RR~~LC~~HEDVEALAAIY 239
 |||||
 311 SSLPPNNSYADFERFSKVL~~EE~~AAAAEEGLRELQ~~RS~~RR~~LC~~HEDVEALAAIY 360
 |||||
 240 EEKEAWYREESDSL~~GQ~~DLRRLRQ~~ELL~~KT~~EA~~LK~~RO~~AQ~~EE~~AKGALLGTSGLK 289
 |||||
 361 EEKEAWYREESDSL~~GQ~~DLRRLRQ~~ELL~~KT~~EA~~LK~~RO~~AQ~~EE~~AKGALLGTSGLK 410
 |||||
 290 RRF~~S~~RL~~N~~RYEALAKQVASEMRFVQDLVRALEQ~~E~~KLQGV~~EC~~GLR 333
 |||||
 411 RRF~~S~~RL~~N~~RYEALAKQVASEMRFVQDLVRALEQ~~E~~KLQGV~~EC~~GLR 454
 |||||

FIG. 56

61 GETALHKAACQRNRAVCQLLLVDAGASLRKTD SKGKTPQERAQQAGDPDLA 110
 |||||
 995 GETALHKAACQRNRAVCQLLLVDAGASLRKTD SKGKTPQERAQQAGDPDLA 1044
 .
 111 AYLESRQNYKVIGHEDLETAV 131
 |||||
 1045 AYLESRQNYKVIGHEDLETAV 1065

FIG. 57

```

1 MRGAARLGRPGRSCLPALRAPRPPLLLLLALLPLLPAPGAAAAPAPR 50
  ||||| ||||| ||||| | |||| : | | || ||
1 MRGAARLGRPGRSCLPALRAAAP..ALLARCAVAAAAGLRAAARPR 48

51 PPELQASAGPSVSLYLSEDEVRRRLIGLDAELYVVRNDLISHYALSFSLL 100
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||
49 PPELQASAGPSVSLYLSEDEVRRRLIGLDAELYVVRNDLISHYALSFNLL 98

101 VPSETNFLHFTWHAKSKVEYKLGFGQVDNVLAMDMPQVNISVQGEVPRTLS 150
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
99 VPSETNFLHFTWHAKSKVEYKLGFGQVDNVLAMDMPQVNISVQGEVPRTLS 148

151 VFRVELSCTGKVDSEVMILMQNLNTVNSSKNFTVLNFKRRKMCYKKLEEV 200
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
149 VFRVELSCTGKVDSEVMILMQNLNTVNSSKNFTVLNFKRRKMCYKKLEEV 198

201 KTSALDKNTSRTIYDPVHAAPTSTRVFYISVGVCCAVIFLVAIILAVLH 250
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
199 KTSALDKNTSRTIYDPVHAAPTSTRVFYISVGVCCAVIFLVAIILAVLH 248

251 LHSMKRIELDD 261
  ||:|||||||
249 LHNMKRIELDD 259

```

၆၆

1 MPQVNISVQGEVPRTL SVFRVELSCTGKVDSEVMILMQNLTVNSSKNFT 50
 |||||
 132 MPQVNISVQGEVPRTL SVFRVELSCTGKVDSEVMILMQNLTVNSSKNFT 181
 . . .
 51 VLNFKRRKMCYKKLEEVKTSALDKNTSRTIYDPVHAAPTSTRVFYISVG 100
 |||||
 182 VLNFKRRKMCYKKLEEVKTSALDKNTSRTIYDPVHAAPTSTRVFYISVG 231
 . . .
 101 VCCAVIFLVAIILAVLHLHSMKRIELDDSIASSSSQGLSQPSTQTTQYL 150
 |||||:|||||
 232 VCCAVIFLVAIILAVLHLHSMKRIELDDSIASSSSQGLSQPSTQTTQYL 281
 . . .
 151 RADTPNNA TPITSSYYPTLRIEKNDLRSVTLLEAKGKVKDIAISRERITL 200
 |||||
 282 RADTPNNA TPITS..YPTLRIEKNDLRSVTLLEAKGKVKDIAISRERITL 329
 . . .
 201 KDV LQEGTFGRIFHGILIDEKDPNKEKQAFVKTVKDQASEIQVTMMLTES 250
 |||||
 330 KDV LQEGTFGRIFHGILIDEKDPNKEKQAFVKTVKDQASEIQVTMMLTES 379

FIG. 59

251 CKLRGLHHRNLLPITHVCIEEGEKEKPMVILPYMWNWGNLKLFLRQCKLVEAN 300
 |||||
 380 CKLRGLHHRNLLPITHVCIEEGEKEKPMVILPYMWNWGNLKLFLRQCKLVEAN 429
 301 NPQAISQQDLVHMAIQIACGMSYLARREVIHKDLAARNVCV 340
 |||||
 430 NPQAISQQDLVHMAIQIACGMSYLARREVIHKDLAARNVCV 469

FIG. 59 (CONT.¹)

1 MEAIRTDNQNFASQLREAEARNRDLEAHVRQLQERMELLQAEGATAVTGV 50
 |||||
 484 MEAIRTDNQNFASQLREAEARNRDLEAHVRQLQERMELLQAEGATAVTGV 533
 .
 51 PSPRATDPPSHL.....DGPPAVAVGCQCLVGP.GPMHRRHL 86
 |||||
 534 PSPRATDPPSHMAPRPWLWASARWWGQAPCTAATCCSLPGSLGLAYRR.. 581
 .
 87 LLPARVP...RPGLSEALSLLLFAVVLSRAAALGCIGLVAHAGQLTAVWR 133
 || | ||:| ||| |:: |
 582RFPCSCSP.....LFCLVPPPPWAAALGWWPTPANSPQ..... 612
 .
 134 RPGAARAP 141
 |||: |
 613 .SGAAQEP 619

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FIG. 60

```

1  MELLQAEGATAVTGVSPRATDPPSHL.....DGPPAVAVGQ 37
   |||||
519 MELLQAEGATAVTGVSPRATDPPSHMAPRPWLWASARWWGQAPCTAATC 568
      |::|:

38  CPLVGP.GPMHRRHLLPARVP...RPGLSEALSLLLFAVVLRSAAALGC 83
   | | | | : | | | | | | | | | | | | | | | | | | |
569 CSLPGSLGLAYRR.....RFPCSCSP.....LFCLVPPPPWAALGW 603

84  IGLVAHAGQLTAVWRRRPGAARAP 106
   |::| | | | | | | | | | | | | | | | | | | | | | |
604 WPTPANSPQ.....SGAAQEP 619

```

FIG. 61

FIG. 62

```

1 MARTSQLYDAVPIQSSVVLCSPPSPMVRTQTESSTPPGIPGGSRQGP 50
  |||
1 MARTSQLYDAVPIQSSVVLCSPPSPMVRTQTESSTPPGIPGGSRQGP 50
  |||

51 MDGTAAEPRPGAGSLQHAQPPQPRKKRPEDFKFGKILGEGSFSTVVLAR 100
  |||
51 MDGTAAEPRPGAGSLQHAQPPQPRKKRPEDFKFGKILGEGSFSTVVLAR 100
  |||

101 ELATSREYAIKILEKRHI IKENKVPYVTRERDVMSRLDHPFFVKLYFTFQ 150
  |||
101 ELATSREYAIKILEKRHI IKENKVPYVTRERDVMSRLDHPFFVKLYFTFQ 150
  |||

151 DDEKLYFGLSYAKNGELLKYIRKIGSFDETCTRFYTAIEIVSALEYLHGKG 200
  |||
151 DDEKLYFGLSYAKNGELLKYIRKIGSFDETCTRFYTAIEIVSALEYLHGKG 200
  |||

201 IIHRDLKPENILLNEDMHIQITDFGTAKVLSPEKQ 236
  |||
201 IIHRDLKPENILLNEDMHIQITDFGTAKVLSPEKQ 236
  |||

```

FIG. 63

```
51 LNNFSVASSVMFR 63
    |||||: ::
51 LNNFSVAKCQLMK 63
```

FIG. 64

```

1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLLLKTDGSFIGYKEKPQDVDLPYP 50
  |||||
1 MSDVTIVKEGWVQKRGEYIKNWRPRYFLLLKTDGSFIGYKEKPQDVDLPYP 50

51 LNNFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPEREETE 100
  |||||
51 LNNFSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPEREETE 100

101 AIQAVADRLQRQEEERMNCSPSTSQIDNIGEEEMDASTHHKRKTMNDFDY 150
  |||||
101 AIQAVADRLQRQEEERMNCSPSTSQIDNIGEEEMDASTHHKRKTMNDFDY 150

151 LKLLGKGTFGKVILVREKASGKYAMKILKKEVIAK 187
  |||||
151 LKLLGKGTFGKVILVREKASGKYAMKILKKEVIAK 187

```

FIG. 65

[illegible]

FIG. 66

FIG. 67

FIG. 68



```

1 MGHALCVCSRGTVIIDNKRYLFIQKLGE GFSYVDLVEGLHDGHFYALKR 50
  |||||
1 MGHALCVCSRGTVIIDNKRYLFIQKLGE GFSYVDLVEGLHDGHFYALKR 50

51 ILCHEQQDREEAQREADMHRLFNHPNII LRLVAYCLRERGAKHEAWLLPF 100
  |||||
51 ILCHEQQDREEAQREADMHRLFNHPNII LRLVAYCLRERGAKHEAWLLPF 100

```

101 FK 102

101 FK 102

FIG. 70

```

1  MERAI SPGLLVRA LLLLLLLGLAARTVAAGRARGLPAPTAAEAFGLGAAA 50
  |||||
1  MERAI SPGLLVRA LLLLLLLGLAARTVAAGRARGLPAPTAAEAFGLGAAA 50

51  APTSA TRVPAAGAVAAA ETVEDA EALPAAAGEQEP RGPEDDET ELP R 100
  |||||
51  APTSA TRVPAAGAVAAA ETVEDA EALPAAAGEQEP RGPEDDET ELP R 100

101 GRSLV IISTLDGR IAAALDPENHGKKQWDLDVGGSLVSSSLSKPEVFGNK 150
  |||||
101 GRSLV IISTLDGR IAAALDPENHGKKQWDLDVGGSLVSSSLSKPEVFGNK 150

151 MII PSLDGALFQWDRDR ESME TVPFTVESLLES SYKFGDDVVLVGGKSLT 200
  |||||
151 MII PSLDGALFQWDRDR ESME TVPFTVESLLES SYKFGDDVVLVGGKSLT 200

```

FIG. 71

201 TYGLSAYSGKVRYICSALGCRQWSDMEQEEDILLQRTQKTAVGPR 250
 |||||
 201 TYGLSAYSGKVRYICSALGCRQWSDMEQEEDILLQRTQKTAVGPR 250
 .
 251 SGNEKWNFSVGHFELRYIPDMETRAGFIESTFKPNENTEESKIISDVEEQ 300
 |||||
 251 SGNEKWNFSVGHFELRYIPDMETRAGFIESTFKPNENTEESKIISDVEEQ 300
 .
 301 EAAIMDIVIKVSVADWKVMAFSKKGHLEWEYQFCTPIASAWLLKDGV 350
 |||||
 301 EAAIMDIVIKVSVADWKVMAFSKKGHLEWEYQFCTPIASAWLLKDGV 350
 .
 351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENSVYLGMYRGQLYLQSSV 400
 |||||
 351 PISLFDDTSYTSNDDVLEDEEDIVEAARGATENSVYLGMYRGQLYLQSSV 400
 .
 401 RISEKFPSPKALESVTNENAIIPPTIKWKPLIHSPSRTPVLVGSDEFD 450
 |||||
 401 RISEKFPSPKALESVTNENAIIPPTIKWKPLIHSPSRTPVLVGSDEFD 450

FIG. 71 (CONT.¹)

451	KCLSNDKFSHEEYSNGALSILQPYDNGYLYLPYKRNKRSTQITVRFL	500
451	KCLSNDKFSHEEYSNGALSILQPYDNGYLYLPYKRNKRSTQITVRFL	500
501	DNPHYNKNIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLEFHPHPRQ	550
501	DNPHYNKNIRKKDPVLLHWWKEIVATILFCIIATTFIVRRLEFHPHPRQ	550
551	RKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPIQCLGR	600
551	RKESETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPIQCLGR	600
601	GGFGVVFEAKNKVDDCNYAIKRIRLPNRELAREKVMREVKALAKLEHPGI	650
601	GGFGVVFEAKNKVDDCNYAIKRIRLPNRELAREKVMREVKALAKLEHPGI	650
651	VRYFNAWLEAPPEKWQEKMDIWLKDESTDWPLSSPSPMDAPSVKIRMD	700
651	VRYFNAWLEAPPEKWQEKMDIWLKDESTDWPLSSPSPMDAPSVKIRMD	700

FIG. 71 (CONT. 2)

701 PFSTKEHIEIIAPSPQRSRFSVIGISCDQTSSSESQFSPLEFSGMDHEDI 750
|||||
701 PFSTKEHIEIIAPSPQRSRFSVIGISCDQTSSSESQFSPLEFSGMDHEDI 750
751 SESVDAAYNLQDSCLTDCDVEDGTMDGNDEGHSEFELCPSEASPYVRSRER 800
|||||
751 SESVDAAYNLQDSCLTDCDVEDGTMDGNDEGHSEFELCPSEASPYVRSRER 800
801 TSSSIVFEDSGCDNASSKEPKTNRLHIGNHCANKLT 837
|||||
801 TSSSIVFEDSGCDNASSKEPKTNRLHIGNHCANKLT 837

FIG. 71 (CONT.³)


```

1 MGSRAQKSAGNAELWEPLPEGRPRPAGTSSAVSAWASLKLCLRGSGRRQ 50
  |||||
1 MGSRAQKSAGNAELWEPLPEGRPRPAGTSSAVSAWASLKLCLRGSGRRQ 50

51 RLGGRMQPEEGHRLAAGAAVRGAAATVLLRLRDDLNVTLSHFYVKNE 100
  |||||
51 RLGGRMQPEEGHRLAAGAAVRGAAATVLLRLRDDLNVTLSHFYVKNE 100

101 DLEKIGMRPGQRRLWEAVKRRKALCKRKSWMNKVFSGKRLEAEFPPHHS 150
  |||||
101 DLEKIGMRPGQRRLWEAVKRRKALCKRKSWMNKVFSGKRLEAEFPPHHS 150

151 QSTFRKTSPAPGGPAGEPLQSLTCLIGEKLRLLEKLGDSFGVVRGE 200
  |||||
151 QSTFRKTSPAPGGPAGEPLQSLTCLIGEKLRLLEKLGDSFGVVRGE 200

201 WDAPSGKTVS..... 210
  |||||
201 WDAPSGKTVSAVKCLKPDVLSQPEAMDDFIREVNAMHSLDHRNLIRLYG 250

```

FIG. 72

```

210 ..... 210
251 VLTTPMKMVTTELAPLGSLLDRLRKHQHFLGLTSLRYAVQVAEGMGYLE 300
210 ..... 210
301 SKRFIHRDLAARNLLATRDLVKIGDFGLMRALPQNDHVMQEHKVPF 350
210 ..... 210
351 AWCAPESLKTRTFSHASDTWMFGVTLWEMFTYGQEPWIGLNGSQILHKID 400
210 ..... 210
401 KEGERLPRPEDCPQDIYNVMVQCWAHKPEDRPTFVALRDFLLEAQPTDMR 450

```

FIG. 72 (CONT.¹)

FIG. 72 (CONT.)

FIG. 72 (CONT.)

348 DDFEICSINSTLVGAGVPAGPSQGQNTNYAFVPEQARPPPPLEDNLFPPQ 397
 |||||
 698 DDFEICSINSTLVGAGVPAGPSQGQNTNYAFVPEQARPPPPLEDNLFPPQ 747
 |||||
 398 GGGKPPSSAQTAEIFQALQOECMRQLQAPAGSPAPSPGGDDKPQVPPR 447
 |||||
 748 GGGKPPSSAQTAEIFQALQOECMRQLQAP.GSPAPSPGGDDKPQVPPR 796
 |||||
 448 VPIPPRTRPHVQLSPAPPGEEETSQWPGPASPPRVPPREPLSPQGS RTP 846
 |||||
 797 VPIPPRTRPHVQLSPAPPGEEETSQWPGPASPPRVPPREPLSPQGS RTP 547
 |||||
 498 SPLVPPGSSPLPRLSSSPGKTMPTTQSFASDPKYATPQVIQAPGPRAGP 895
 |||||
 847 SPLVPPGSSPLPRLSSSPGKTMPTTQSFASDPKYATPQVIQAPG 597
 |||||
 548 CILPIVRDGKKVSSSTHYLLPERPSYLYRYQRFLEAQSPPEPTPLPVPL 945
 |||||
 896 CILPIVRDGKKVSSSTHYLLPERPSYLYRYQRFLEAQSPPEPTPLPVPL

FIG. 72 (CONT.³)

```

598 LLPPSTPAPAAPTATVRPMPQAAALDPKANFSTNNSNPGARPPPPRATAR 647
|||||
946 LLPPSTPAPAAPTATVRPMPQAAALDPKANFSTNNSNPGARPPPPRATAR 995

648 LPQRCPCPDGPEAGRPADKIQMAMVHGVTTEECQAAALQCHGWSVQACPV 697
|||||
996 LPQRCPCPDGPEAGRPADKIQMAMVHGVTTEECQAAALQCHGWSVQACPV 1045

698 SEGGAALRAGSAAQRECHKVLEMFWDWNLEQAGCHLLGSWGPAHHR 743
|||||
1046 SEGGAALRAGSAAQRECHKVLEMFWDWNLEQAGCHLLGSWGPAHHR 1091

```

FIG. 72 (CONT.⁴)

```

1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLFSDTMVQQKLDIDK 50
  |||||
1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLFSDTMVQQKLDIDK 50

51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNIIKKSNKKLEELHHKL 100
  |||||
51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDNIIKKSNKKLEELHHKL 100

101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCSTSNRLKALQKQLDIELK 150
  |||||
101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCSTSNRLKALQKQLDIELK 150

151 VKQGAENMIQMYSNGSSKDRKLHGTAQQLQDSKTKIEVIRMQILQAVQT 200
  |||||
151 VKQGAENMIQMYSNGSSKDRKLHGTAQQLQDSKTKIEVIRMQILQAVQT 200

201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAEGAKNVMKLLGSGKVTD 250
  |||||
201 NELAFDNAKPVISPLELRMEELRHHFRIEFAVAEGAKNVMKLLGSGKVTD 250

251 RKALSEAQAARFNESSQKLDLLKYSLEQRLNEVPKNHPKSRIIEELSVA 300
  |||||
251 RKALSEAQAARFNESSQKLDLLKYSLEQRLNEVPKNHPKSRIIEELSVA 300

```

FIG. 73

301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRMLGQCQDILENVPGRSK 350
 |||||
 301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRMLGQCQDILENVPGRSK 350
 . . .
 351 ATSVALPGWSPSETRSSFMSTRSKSGSSRNLLKTDDLNDVCAVLKLD 400
 |||||
 351 ATSVALPGWSPSETRSSFMSTRSKSGSSRNLLKTDDLNDVCAVLKLD 400
 . . .
 401 NTVVGQTSWKPISNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
 |||||
 401 NTVVGQTSWKPISNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
 . . .
 451 LEDFLDNQRHGMCLYLEPQGTLEAEVTFNPNVIERPKLQKQKIFSKQQ 500
 |||||
 451 LEDFLDNQRHGMCLYLEPQGTLEAEVTFNPNVIERPKLQKQKIFSKQQ 500
 . . .
 501 GKTFLRAPQMNIATWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
 |||||
 501 GKTFLRAPQMNIATWGRLVRRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
 . . .
 551 IPQLAPPA 558
 |||||
 551 IPQLAPPA 558

FIG. 73 (CONT.¹)

1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLD FSDTMVQKLD DIK 50
|||||
1 MASNPERGEILLTELQGDSRSLPFSENVSAVQKLD FSDTMVQKLD DIK 50

51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDN I LKKS NKLEELH HKL 100
|||||
51 RIKREIRKELKIKEGAENLRKVTTDKKSLAYVDN I LKKS NKLEELH HKL 100

101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCST SNNRLKALQKQLD IELK 150
|||||
101 QELNAHIVVSDPEDITDCPRTPTDTPNNDPRCST SNNRLKALQKQLD IELK 150

151 VKQGAENMIQY SNGSKDRKLHGTAQQLQDSKT KIEVIRMQILQAVQT 200
|||||
151 VKQGAENMIQY SNGSKDRKLHGTAQQLQDSKT KIEVIRMQILQAVQT 200

201 NELAFD NAKPVISPLELRMEELRHHFR IEF A VAE GAKNVMKLLGSGKVTD 250
|||||
201 NELAFD NAKPVISPLELRMEELRHHFR IEF A VAE GAKNVMKLLGSGKVTD 250

FIG. 74


```

251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIIEELSVA 300
    |||||
251 RKALSEAQARFNESSQKDLLKYSLEQRLNEVPKNHPKSRIIIEELSVA 300

301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCCQDILENVPGRSK 350
    |||||
301 ASPTLSPRQSMISTQNQYSTLSKPAALTGTLEVRIMGCCQDILENVPGRSK 350

351 ATSVALPGWSPSETRSSFMSRTSKSKGSSRNLLKTDDLNDVCAVLKLD 400
    |||||
351 ATSVALPGWSPSETRSSFMSRTSKSKGSSRNLLKTDDLNDVCAVLKLD 400

401 NTVVGQTSWKPI SNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450
    |||||
401 NTVVGQTSWKPI SNQSWDQKFTLELDRSRELEISVYWRDWRSLCAVKFLR 450

```

FIG. 74 (CONT.¹)

```

451 LEDFLDNQRHGMCLYLEPQGTLEAEVTFEFPVIERRQKQKIFSKQ 500
|||||
451 LEDFLDNQRHGMCLYLEPQGTLEAEVTFEFPVIERRQKQKIFSKQ 500
|||||

501 GKTFLRAPQMNINIAWGRVLRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
|||||
501 GKTFLRAPQMNINIAWGRVLRRAIPTVNHSGTFSPQAPVPTTVPVVDVR 550
|||||

551 IPQLAPPASDSTVTKLDFDLEPEPPAPPASSLGEIDESSSELRLVDIPG 600
|||||
551 IPQLAPPASDSTVTKLDFDLEPEPPAPPASSLGEIDESSSELRLVDIPG 600

601 QAS 603
|||
601 QDS 603

```

FIG. 74 (CONT.²)

```

1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50
  |||||
1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50

51 TSELLGEGAYAKVQGA VSLQNGKEYAVKII EKQAGHSRSRVFRE VETLYQ 100
  |||||
51 TSELLGEGAYAKVQGA VSLQNGKEYAVKII EKQAGHSRSRVFRE VETLYQ 100

101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGT 131
  |||||
101 CQGNKNILELIEFFEDDTRFYLVFEKLQGGG 131

```

FIG. 75

63 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 112
 |||||
 1 MVSSQKLEKPIEMGSSEPLPIADGDRRRKKRRGRATDSLPGKFEDMYKL 50
 .
 113 TSELLGEGAYAKVQGA VSLQNGKEYAVKV 141
 |||||
 51 TSELLGEGAYAKVQGA VSLQNGKEYAVKI 79

FIG. 76

```

1 MSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDL 50
:|||||
194 LGSGMKLNNSCTPITTPELTTPCGSAEYMAPEVVEVFTDQATFYDKRCDL 243

. . .
51 WSLGVVLYIMLSGYPFVGHCGADCGWDRGEVCRVCQNKLFESI QEGKYE 100
|||||
244 WSLGVVLYIMLSGYPFVGHCGADCGWDRGEVCRVCQNKLFESI QEGKYE 293

. . .
101 FPDKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVQGQAPEKGLP 150
|||||
294 FPDKDWAHISSEAKDLISKLLVRDAKQRLSAAQVLQHPWVQGQAPEKGLP 343

. . .
151 TPQVLQRNSSTMDLTLFAAEAIALNRQLSQHEENELAEPEALADGLCSM 200
|||||
344 TPQVLQRNSSTMDLTLFAAEAIALNRQLSQHEENELAEPEALADGLCSM 393

. . .
201 KLSPPCKSRLARRRALAQAGGEDRSPP TAL 231
|||||
394 KLSPPCKSRLARRRALAQAGGEDRSPP TAL 424

```

FIG. 77

1 MRKGVLKDPEIADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTSEVV 50
 |||||
 1 MRKGVLKDPEIADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTSEVV 50
 . . .
 51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
 |||||
 51 AIKMSYSGKQTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLV 100
 . . .
 101 MEYCLGSASDLLLEVHKKPLQVEVEIAATHGALHGLAYLHSHALIHR 146
 |||||
 101 MEYCLGSASDLLLEVHKKPLQVEVEIAATHGALHGLAYLHSHALIHR 146

FIG. 78

FIG. 79

FIG. 80

FIG. 80

[illegible]

FIG. 18

269 RAHSGAAPWQPLAAPSGASAAEQLOQGNQPVESDESLGGLSAAALRSW 318
 |||||
 553 RAHSGAAPWQPLAAPSGASAAEQLOQGNQPVESDESLGGLSAAALRSW 602
 |||||
 319 HLTSCPLDPAPLREAGCPQGDTAGESSWGS GPGSRPTAVEGLALGSSAS 368
 |||||
 603 HLTSCPLDPAPLREAGCPQGDTAGESSWGS GPGSRPTAVEGLALGSSAS 652
 |||||
 369 SSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSSLPGLGLEQDRQ 418
 |||||
 653 SSSEPPQIIINPARQKMVQKLALYEDGALDSLQLLSSSLPGLGLEQDRQ 702
 |||||

419 GPKKVMNFRA 428
 ||:: :|::

703 GPEESDEFQS 712

FIG. 81 (CONT.¹)

1	MAGPGGPEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFAALIV	50
1	MAGPGGPEPAAPGAQHFLYEVPWVMCRFYKVMDALEPADWCQFAALIV	50
51	RDQTELRLCERSGORTASVLWPWINRNARVADLVHILTHLQLLRARDIIT	100
51	RDQTELRLCERSGORTASVLWPWINRNARVADLVHILTHLQLLRARDIIT	100
101	AWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSSASTFLSPAFFGS	150
101	AWHPPAPLPSPGTTAPRPSSIPAPAEAEAWSPRKLPSSASTFLSPAFFGS	150
151	QTHSGPELGLVPSASLWPPPPSPAPSSTKPGPESSVLLQGARPSPFCW	200
151	QTHSGPELGLVPSASLWPPPPSPAPSSTKPGPESSVLLQGARPSPFCW	200

FIG. 82

```

201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMRNTVYAVKRLKENADLEWT 250
    |||||
201 PLCEISRGTHNFSEELKIGEGGFCVYRAVMRNTVYAVKRLKENADLEWT 250
    |||||
251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
    |||||
251 AVKQSFLTEVEQLSRFRHPNIVDFAGYCAQNGFYCLVYGFLPNGSLEDRL 300
    |||||
301 HCQTQACPPPLSWPQRLDILLGTARASQVSCNRVSSCVSKSSPGL 344
    |||||
301 HCQTQACPPPLSWPQRLDILLGTARAIQF.....LHQDSPSL 336
    |||||

```

FIG. 82 (CONT.¹)

1 MFTEEDVKFYLAELALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFG 50
 |||||
 164 MFTEEDVKFYLAELALDHLHSLGIIYRDLKPENILLDEEGHIKLTDFG 213
 .
 51 LSKESIDHEKKAYSFCGTVEYMAPEVNVNRRGHTQSADWWSFGVLMFEMLT 100
 |||||
 214 LSKESIDHEKKAYSFCGTVEYMAPEVNVNRRGHTQSADWWSFGVLMFEMLT 263
 .
 101 GTLPFQGKDRKETMTMILKAKLGMPQFLSPEAQSLRLMLFKRNPANRLGA 150
 |||||
 264 GTLPFQGKDRKETMTMILKAKLGMPQFLSPEAQSLRLMLFKRNPANRLGA 313
 .
 151 GPDGVEEIKRHSFFSTIDWNKLYRREIHPPFKPATGRPEDTFYFDPEFTA 200
 |||||
 314 GPDGVEEIKRHSFFSTIDWNKLYRREIHPPFKPATGRPEDTFYFDPEFTA 363
 .
 201 KTPKDSPGIPPSANAHQLFRGFSFVAITSDDESQAMQTVGVHHSIVQQLHR 250
 |||||
 364 KTPKDSPGIPPSANAHQLFRGFSFVAITSDDESQAMQTVGVHHSIVQQLHR 413
 .
 251 NSIQFTDGYEVKEDIGVGSYSVCKRCIHKATNMEFAVKV 289
 |||||:
 414 NSIQFTDGYEVKEDIGVGSYSVCKRCIHKATNMEFAVKI 452

FIG. 83

1 MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEEINPQTEEVSIKEI 50
 |||||
 1 MPLAQLADPWQKMAVESPSDSAENGQQIMDEPMGEEEEINPQTEEVSIKEI 50
 . . .
 51 AITHHVKEGHEKADPSQFELLKVLGQGSFGKVFLVKKISGSDARQLYAMK 100
 |||||
 51 AITHHVKEGHEKADPSQFELLKVLGQGSFGKVFLVKKISGSDARQLYAMK 100
 . . .
 101 VLKATLKVDRDRVRTKMERDILVEVNHPPFIVKLHYAFQTEGKLYLILDFL 150
 |||||
 101 VLKATLKVDRDRVRTKMERDILVEVNHPPFIVKLHYAFQTEGKLYLILDFL 150
 . . .
 151 RGGDLFTRLSKEVMFTEEDVKFYLAELALALDHLHSLGIYYRDLKPE 197
 |||||
 151 RGGDLFTRLSKEVMFTEEDVKFYLAELALALDHLHSLGIYYRDLKPE 197

FIG. 84

1 MSTEADEGITFSVPPFAPSGFCTIPEGGICRRGGAAAVGEGEEHQLPPPP 50
 |||||
 1 MSTEADEGITFSVPPFAPSGFCTIPEGGICRRGGAAAVGEGEEHQLPPPP 50
 |||||
 51 PGSEWNVESAAAPGIGCPAATSSSSATRGRGSSVGGSRRTTVAYVINEA 100
 |||||
 51 PGSEWNVESAAAPGIGCPAATSSSSATRGRGSSVGGSRRTTVAYVINEA 100
 |||||
 101 SQQLVVAESEALQSLREACETVGATLETLHFGKLDFGETTVLDRFYNAD 150
 |||||
 101 SQQLVVAESEALQSLREACETVGATLETLHFGKLDFGETTVLDRFYNAD 150
 |||||
 151 IAVVEMSDAFRQPSLFYHLGVRESFSMANNIILYCDTNSDSLQSLKEIIC 200
 |||||
 151 IAVVEMSDAFRQPSLFYHLGVRESFSMANNIILYCDTNSDSLQSLKEIIC 200
 |||||
 201 QKNTMCTGNYTFVPYMITPHNKVYCCDSSFMMKGLTELMQPNFELLGPIC 250
 |||||
 201 QKNTMCTGNYTFVPYMITPHNKVYCCDSSFMMKGLTELMQPNFELLGPIC 250
 |||||

FIG. 85

251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
 |||||
 251 LPLVDRFIQLLKVAQASSQYFRESILNDIRKARNLYTGKELAAELARIR 300
 |||||
 301 QRVDNIEVLTADIVINLLSYRDIQDYDSIVKLVEKLPFTFDLASHHH 350
 |||||
 301 QRVDNIEVLTADIVINLLSYRDIQDYDSIVKLVEKLPFTFDLASHHH 350
 |||||
 351 VKFHYAFALNRRNLPGDRAKALDIMIPMVQSEGQVADMYCLVGRIYKDM 400
 |||||
 351 VKFHYAFALNRRNLPGDRAKALDIMIPMVQSEGQVADMYCLVGRIYKDM 400
 |||||
 401 FLDSNFTDTESRDHGASWFKKAFESEPTLQSGINYAVLLLAAGHQFESSF 450
 |||||
 401 FLDSNFTDTESRDHGASWFKKAFESEPTLQSGINYAVLLLAAGHQFESSF 450
 |||||
 451 ELRKVG 456
 |||||
 451 ELRKVG 456

FIG. 85 (CONT.¹)

FIG. 86

```
68 IGS.....AAYDAVLDNRNVAIKKLSRPFQNTAKRAYRELVLMLKCVN 110  
    |||      ||||| ||||| ||||| ||||| ||||| ||||| |||||  
70 IGGAQGIVCAAYDAVLDNRNVAIKKLSRPFQNTAKRAYRELVLMLKCVN 119  
  
111 HKNIISLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQMELDHERMSYL 160  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
120 HKNIISLLNVFTPQKTLEEFQDVYLVME LMDANLCQVIQMELDHERMSYL 169  
  
161 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFM 210  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
170 LYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFM 219  
  
211 MTPYVVTRYRAPEVILGMGYKENVDIWSVGCI MGEMVRHKILFPGRDYI 260  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
220 MTPYVVTRYRAPEVILGMGYKENVDIWSVGCI MGEMVRHKILFPGRDYI 269  
  
261 DQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLT FPKLFPDSLFP 310  
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
270 DQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLT FPKLFPDSLFP 319
```

FIG. 78

311 ADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVE 360
 |||||
 320 ADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVE 369
 361 APPPQIYDKQLDERHTIEEWKELIYKEVMNSEKTKNGVVKGPSPSAQ 410
 |||||
 370 APPPQIYDKQLDERHTIEEWKELIYKEVMNSEKTKNGVVKGPSPSAQ 419

411 VQQ 413

|||

420 VQQ 422

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FIG. 87 (CONT.¹)

```

1  MSKSKVDNQFYSEVEVDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDR 50
   |||||
39 MSKSKVDNQFYSEVEVDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDR 88
   . . . . .
51 NVAIKKLSRPFQÑTHAKRAYRELVLKMCVNHKNV..... 85
   |||||
89 NVAIKKLSRPFQÑTHAKRAYRELVLKMCVNHKNIIISLNVFTPPQKTLEE 138
   .
      86 ...SEVIFKLLAVGVCKI 100
         :::::|: ::::|:
      139 FQDVYLVMEI LMDANLCQV 156

```

FIG. 88

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```

1 MAMTGSTPCSSMSNHTKERVTMTKVTLENFYSNLIAQHEEREMRQKKLEK 50
  |||||
1 MAMTGSTPCSSMSNHTKERVTMTKVTLENFYSNLIAQHEEREMRQKKLEK 50

51 VMEEGLKDEEKRLRRSAHARKETEFRLKRTLGLGFESLKVIGRGAF 100
  |||||
51 VMEEGLKDEEKRLRRSAHARKETEFRLKRTLGLGFESLKVIGRGAF 100

101 GEVRLVQKKDTGHVYAMKILRKADMLEKEQVGHIRAERDILVEADSLWVV 150
  |||||
101 GEVRLVQKKDTGHVYAMKILRKADMLEKEQVGHIRAERDILVEADSLWVV 150

151 KMFYSFQDKLNLYLIMEFLPGGDMTLLMKKDTLTHEEETQFYIAETVLAI 200
  |||||
151 KMFYSFQDKLNLYLIMEFLPGGDMTLLMKKDTLTHEEETQFYIAETVLAI 200

201 DSIHQLGFIHRDIKPDNLLDSKGVKLSDFGLCTGLKKAHRTEFYRNLN 250
  |||||
201 DSIHQLGFIHRDIKPDNLLDSKGVKLSDFGLCTGLKKAHRTEFYRNLN 250

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FIG. 89

251 HSLPSDFTFQNMNSKRKAETWKRNRRLAFTVGTPDYIAPEVFMQTGYN 300
|||||
251 HSLPSDFTFQNMNSKRKAETWKRNRRLAFTVGTPDYIAPEVFMQTGYN 300

301 KLCDWWSLGVIMYEMMLIG 318
|||||
301 KLCDWWSLGVIMYEMMLIG 318

FIG. 89 (CONT.¹)

11 VSGGSMLDIIKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 60
:|||||
143 LSGGSMLDIIKYIVNRGEHKNVLEEAIATILKEVLEGLDYLHRNGQIH 192

61 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVVRKTFVGTPCWMA 110
|||||
193 RDLKAGNILLGEDGSVQIADFGVSAFLATGGDVTRNKVVRKTFVGTPCWMA 242

111 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLM LTLQNDP 160
|||||
243 PEVMEQVRGYDFKADMWSFGITAIELATGAAPYHKYPPMKVLM LTLQNDP 292

161 PLETGVEDKEMMKYKGSFRKLLSLCLQKDP SKRPTAAELLKCKFFQKA 210
|||||
293 PLETGVEDKEMMKYKGSFRKLLSLCLQKDP SKRPTAAELLKCKFFQKA 342

211 KNREYLI EKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDMD 260
|||||
343 KNREYLI EKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWESDDMD 392

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FIG. 90

261 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEQIQSLSVHDSQGPNA 310
 |||||
 393 EKSEEGKAAFSQEKSRVKEENPEIAVSASTIPEQIQSLSVHDSQGPNA 442
 |||||
 311 NEDYREASSCAVNLVLRNRSRKELNDIRFEFTPGRDTADGVSQELFSAG 360
 |||||
 443 NEDYREASSCAVNLVLRNRSRKELNDIRFEFTPGRDTADGVSQELFSAG 492
 |||||
 361 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFA 410
 |||||
 493 LVDGHDVVIVAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFA 542
 |||||
 411 QLSVS 415
 |||||
 543 QLSVS 547

FIG. 90 (CONT.¹)

16. H. H.

261	EKSEEGKA	AFSQEK	SRVKEEN	PEIAVS	ASTIPE	QIQSL	SVHDS	QGP	PNA	310
393	EKSEEGKA	AFSQEK	SRVKEEN	PEIAVS	ASTIPE	QIQSL	SVHDS	QGP	PNA	442
311	NEDYREAS	SCAVNL	VLRLNR	SRKELN	DIRFEFT	PGRDT	ADGV	SQEL	FSAG	360
443	NEDYREAS	SCAVNL	VLRLNR	SRKELN	DIRFEFT	PGRDT	ADGV	SQEL	FSAG	492
361	LVDGHD	VVIVA	ANLQK	IVDDP	KALK	TLT	FKL			391
493	LVDGHD	VVIVA	ANLQK	IVDDP	KALK	TLT	FKL			523

FIG. 91 (CONT.¹)